

# RAW SEQUENCE LISTING

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Application Serial Number: 10/780,703A  
Source: 1Fw/b  
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IFW16

## RAW SEQUENCE LISTING

DATE: 10/13/2006

PATENT APPLICATION: US/10/780,703A

TIME: 15:36:47

Input Set : A:\06-10-06.ST25.txt

Output Set: N:\CRF4\10132006\J780703A.raw

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3 <110> APPLICANT: Lee, Jong Seob
4      Kim, Yun Hee
5      Choi, Eun kyung
6      Yoo, So Yeon
7      Ahn, Ji Hoon
8      Choi, Yang Do
10 <120> TITLE OF INVENTION: Gene Controlling Flowering Time of Plants and Method for
11      Manipulating Flowering Time of Plant Using the Same
13 <130> FILE REFERENCE: 1012679-000105
15 <140> CURRENT APPLICATION NUMBER: US 10/780,703A
16 <141> CURRENT FILING DATE: 2004-02-19
18 <150> PRIOR APPLICATION NUMBER: KR 10 2003 10772
19 <151> PRIOR FILING DATE: 2003-02-20
21 <160> NUMBER OF SEQ ID NOS: 12
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1140
27 <212> TYPE: DNA
28 <213> ORGANISM: Arabidopsis thaliana
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(1137)
34 <223> OTHER INFORMATION: cDNA of LOV1 gene
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41 gtc aac aat aac gaa aaa ggt ata gaa gac aat gat cat aga ggc ggc      96
42 Val Asn Asn Asn Glu Lys Gly Ile Glu Asp Asn Asp His Arg Gly Gly
43          20          25          30
45 caa gag agt cat gtc caa aat gaa gat gaa gct gat gat cat gat cat      144
46 Gln Glu Ser His Val Gln Asn Glu Asp Glu Ala Asp Asp His Asp His
47          35          40          45
49 gac atg gtc atg ccc gga ttt aga ttc cat cct acc gaa gaa gaa ctc      192
50 Asp Met Val Met Pro Gly Phe Arg Phe His Pro Thr Glu Glu Glu Leu
51          50          55          60
53 ata gag ttt tac ctt cgc cga aaa gtt gaa ggc aaa cgc ttt aat gta      240
54 Ile Glu Phe Tyr Leu Arg Arg Lys Val Glu Gly Lys Arg Phe Asn Val
55 65          70          75          80
57 gaa ctc atc act ttc ctc gat ctt tat cgc tat gat cct tgg gaa ctt      288
58 Glu Leu Ile Thr Phe Leu Asp Leu Tyr Arg Tyr Asp Pro Trp Glu Leu
59          85          90          95
61 cct gct atg gcg gcg ata gga gag aaa gag tgg tac ttc tat gtg cca      336

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62	Pro	Ala	Met	Ala	Ala	Ile	Gly	Glu	Lys	Glu	Trp	Tyr	Phe	Tyr	Val	Pro	
63				100					105					110			
65	aga	gat	cgg	aaa	tat	aga	aat	gga	gat	aga	ccg	aac	cga	gta	acg	act	384
66	Arg	Asp	Arg	Lys	Tyr	Arg	Asn	Gly	Asp	Arg	Pro	Asn	Arg	Val	Thr	Thr	
67			115					120					125				
69	tca	gga	tat	tgg	aaa	gcc	acc	gga	gct	gat	agg	atg	atc	aga	tcg	gag	432
70	Ser	Gly	Tyr	Trp	Lys	Ala	Thr	Gly	Ala	Asp	Arg	Met	Ile	Arg	Ser	Glu	
71		130					135					140					
73	act	tct	cgg	cct	atc	gga	tta	aag	aaa	acc	cta	gtt	ttc	tac	tct	ggt	480
74	Thr	Ser	Arg	Pro	Ile	Gly	Leu	Lys	Lys	Thr	Leu	Val	Phe	Tyr	Ser	Gly	
75	145					150				155					160		
77	aaa	gcc	cct	aaa	ggc	act	cgt	act	agt	tgg	atc	atg	aac	gag	tat	cgt	528
78	Lys	Ala	Pro	Lys	Gly	Thr	Arg	Thr	Ser	Trp	Ile	Met	Asn	Glu	Tyr	Arg	
79				165						170				175			
81	ctt	ccg	cac	cat	gaa	acc	gag	aag	tac	caa	aag	gct	gaa	ata	tca	ttg	576
82	Leu	Pro	His	His	Glu	Thr	Glu	Lys	Tyr	Gln	Lys	Ala	Glu	Ile	Ser	Leu	
83			180						185				190				
85	tgc	cga	gtg	tac	aaa	agg	cca	gga	gta	gaa	gat	cat	cca	tcg	gta	cca	624
86	Cys	Arg	Val	Tyr	Lys	Arg	Pro	Gly	Val	Glu	Asp	His	Pro	Ser	Val	Pro	
87		195					200					205					
89	cgt	tct	ctc	tcc	aca	aga	cat	cat	aac	cat	aac	tca	tcg	aca	tca	tcc	672
90	Arg	Ser	Leu	Ser	Thr	Arg	His	His	Asn	His	Asn	Ser	Ser	Thr	Ser	Ser	
91		210					215					220					
93	cgt	tta	gcc	tta	aga	caa	caa	caa	cac	cat	tca	tcc	tcc	tct	aat	cat	720
94	Arg	Leu	Ala	Leu	Arg	Gln	Gln	Gln	His	His	Ser	Ser	Ser	Ser	Asn	His	
95	225					230					235				240		
97	tcc	gac	aac	aac	ctt	aac	aac	aac	aac	aac	atc	aac	aat	ctc	gag	aag	768
98	Ser	Asp	Asn	Asn	Leu	Asn	Asn	Asn	Asn	Asn	Ile	Asn	Asn	Leu	Glu	Lys	
99				245					250					255			
101	ctc	tcc	acc	gaa	tat	tcc	ggc	gac	ggc	agc	aca	aca	aca	acg	acc	aca	816
102	Leu	Ser	Thr	Glu	Tyr	Ser	Gly	Asp	Gly	Ser	Thr	Thr	Thr	Thr	Thr	Thr	
103			260						265					270			
105	aac	agt	aac	tct	gac	gtt	acc	att	gct	cta	gcc	aat	caa	aac	ata	tat	864
106	Asn	Ser	Asn	Ser	Asp	Val	Thr	Ile	Ala	Leu	Ala	Asn	Gln	Asn	Ile	Tyr	
107		275					280					285					
109	cgt	cca	atg	cct	tac	gac	aca	agc	aac	aac	aca	ttg	ata	gtc	tct	acg	912
110	Arg	Pro	Met	Pro	Tyr	Asp	Thr	Ser	Asn	Asn	Thr	Leu	Ile	Val	Ser	Thr	
111		290					295					300					
113	aga	aat	cat	caa	gac	gat	gat	gaa	act	gcc	att	gtt	gac	gat	ctt	caa	960
114	Arg	Asn	His	Gln	Asp	Asp	Asp	Glu	Thr	Ala	Ile	Val	Asp	Asp	Leu	Gln	
115	305					310				315					320		
117	aga	cta	gtt	aac	tac	caa	ata	tca	gat	gga	gcg	aca	acg	cta	atg	cct	1008
118	Arg	Leu	Val	Asn	Tyr	Gln	Ile	Ser	Asp	Gly	Ala	Thr	Thr	Leu	Met	Pro	
119			325						330				335				
121	caa	act	caa	gcg	gcg	tta	gct	atg	aac	atg	att	cct	gca	gga	acg	att	1056
122	Gln	Thr	Gln	Ala	Ala	Leu	Ala	Met	Asn	Met	Ile	Pro	Ala	Gly	Thr	Ile	
123			340						345				350				
125	cca	aac	aat	gct	ttg	tgg	gat	atg	tgg	aat	cca	ata	gta	cca	gat	gga	1104
126	Pro	Asn	Asn	Ala	Leu	Trp	Asp	Met	Trp	Asn	Pro	Ile	Val	Pro	Asp	Gly	

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127          355          360          365
129 aac aga gat cac tat act aat att cct ttt aag taa
130 Asn Arg Asp His Tyr Thr Asn Ile Pro Phe Lys
131          370          375
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135 <211> LENGTH: 379
136 <212> TYPE: PRT
137 <213> ORGANISM: Arabidopsis thaliana
139 <400> SEQUENCE: 2
141 Met Ala Ile Val Ser Ser Thr Thr Ser Ile Ile Pro Met Ser Asn Gln
142 1          5          10          15
145 Val Asn Asn Asn Glu Lys Gly Ile Glu Asp Asn Asp His Arg Gly Gly
146          20          25          30
149 Gln Glu Ser His Val Gln Asn Glu Asp Glu Ala Asp Asp His Asp His
150          35          40          45
153 Asp Met Val Met Pro Gly Phe Arg Phe His Pro Thr Glu Glu Glu Leu
154          50          55          60
157 Ile Glu Phe Tyr Leu Arg Arg Lys Val Glu Gly Lys Arg Phe Asn Val
158 65          70          75          80
161 Glu Leu Ile Thr Phe Leu Asp Leu Tyr Arg Tyr Asp Pro Trp Glu Leu
162          85          90          95
165 Pro Ala Met Ala Ala Ile Gly Glu Lys Glu Trp Tyr Phe Tyr Val Pro
166          100          105          110
169 Arg Asp Arg Lys Tyr Arg Asn Gly Asp Arg Pro Asn Arg Val Thr Thr
170          115          120          125
173 Ser Gly Tyr Trp Lys Ala Thr Gly Ala Asp Arg Met Ile Arg Ser Glu
174          130          135          140
177 Thr Ser Arg Pro Ile Gly Leu Lys Lys Thr Leu Val Phe Tyr Ser Gly
178 145          150          155          160
181 Lys Ala Pro Lys Gly Thr Arg Thr Ser Trp Ile Met Asn Glu Tyr Arg
182          165          170          175
185 Leu Pro His His Glu Thr Glu Lys Tyr Gln Lys Ala Glu Ile Ser Leu
186          180          185          190
189 Cys Arg Val Tyr Lys Arg Pro Gly Val Glu Asp His Pro Ser Val Pro
190          195          200          205
193 Arg Ser Leu Ser Thr Arg His His Asn His Asn Ser Ser Thr Ser Ser
194          210          215          220
197 Arg Leu Ala Leu Arg Gln Gln Gln His His Ser Ser Ser Ser Asn His
198 225          230          235          240
201 Ser Asp Asn Asn Leu Asn Asn Asn Asn Asn Ile Asn Asn Leu Glu Lys
202          245          250          255
205 Leu Ser Thr Glu Tyr Ser Gly Asp Gly Ser Thr Thr Thr Thr Thr Thr
206          260          265          270
209 Asn Ser Asn Ser Asp Val Thr Ile Ala Leu Ala Asn Gln Asn Ile Tyr
210          275          280          285
213 Arg Pro Met Pro Tyr Asp Thr Ser Asn Asn Thr Leu Ile Val Ser Thr
214          290          295          300
217 Arg Asn His Gln Asp Asp Asp Glu Thr Ala Ile Val Asp Asp Leu Gln
218 305          310          315          320

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221 Arg Leu Val Asn Tyr Gln Ile Ser Asp Gly Ala Thr Thr Leu Met Pro
222             325             330             335
225 Gln Thr Gln Ala Ala Leu Ala Met Asn Met Ile Pro Ala Gly Thr Ile
226             340             345             350
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234             370             375
237 <210> SEQ ID NO: 3
238 <211> LENGTH: 2606
239 <212> TYPE: DNA
240 <213> ORGANISM: Arabidopsis thaliana
243 <220> FEATURE:
244 <221> NAME/KEY: gene
245 <222> LOCATION: (1)..(2606)
246 <223> OTHER INFORMATION: genomic DNA of LOV1 gene
248 <400> SEQUENCE: 3
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251 gaaaaaggta tagaagacaa tgatcataga ggcggccaag agagtcatgt ccaaaatgaa      120
253 gatgaagctg atgatcatga tcatgacatg gtcatgcccg gatttagatt ccacacctacc      180
255 gaagaagaac tcatagagtt ttaccttcgc cgaaaagttg aaggcaaacg ctttaatgta      240
257 gaactcatca ctttctctga tctttatcgc tatgatcctt gggaacttcc tggtaaatat      300
259 acattcacat aaacacacat aaatcatctc aaactatttg gaaatcttaa tttctattca      360
261 tatgttaaga tctttcttct ctcttatcac tttctctctc tatttctttt tttttaacct      420
263 atatatgtac ctacctcctt atgaagtatt actatgtcga tcgttaacaa ttctcaatat      480
265 ctttaaacgc ttctccctct ttagtttctt tcttaatta acctaattaa acaacctaca      540
267 tatatatcat aagatataca aatatgtgta tgttttcata attagcttat gtatgtttaa      600
269 tcatagatat atgtatatgc agctatggcg gcgataggag agaaagagtg gtacttctat      660
271 gtgccaagag atcggaataa tagaaatgga gatagaccga accgagtaac gacttcagga      720
273 tattggaaa ccacggagc tgataggatg atcagatcgg agacttctcg gcctatcgga      780
275 ttaagaaaaa ccctagtgtt ctactctgtt aaagccccta aaggcactcg tactagtgtg      840
277 atcatgaacg agtatcgtct tccgcaccat gaaaccgaga agtaccaaaa ggtataaatt      900
279 ctactataac tctatatata tcctattcat acatacatag atataaccct agctagggtg      960
281 tgaggccttt aaaattgaaa ttaatcccta gacagtttga attttttctt ttttgactag      1020
283 ttttatttat ttattttgga attgattcga taagatcaaa aatacttgtg aatggactaa      1080
285 atgtcaggcg gcgtttgcgc ttaaaccag aaaaatgttc atgtcatatg cgtgaactct      1140
287 ttaaattgct agacatggcc catatgttat agtagaatac attaatagat agatgcatac      1200
289 acatatatat aaacacacaa gtatcacact cgacattcat atacctaat tctgcagaga      1260
291 catagttagt ttttcttaca atttatgaca tgaatgttcc tgctcttctc cacattaatt      1320
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295 ccaacatatt tatatgcgaa catttaaaat ctatacgaat gataacggtt tatggagtag      1440
297 accgaaaaaa tattatgtat acggaaaatg acaatggata gataaataca ttttttgggc      1500
299 tctttcgact tatatgtcgt caccatttga aaccataaat ttataaaatt ttctatgtat      1560
301 atatatgata ttatgatgta tgcataagac agctaaaaca acagggttga cataattatc      1620
303 tatgtgatg tattgcacat tcacttgtac taataaaact aaaattacgc aattaaatat      1680
305 ataaaaaata ataaatataa tcatcttaat tatatttgca ttgttacgtc atatgatagt      1740
307 actctaaatt tcttctaaac gtgctatctt tttttgctaa tgctaacttt acatagtttg      1800
309 tgaatcttct ttcaaaacca tatcttcgat aaatgatatt tttcatagat attgttagtc      1860
311 tatatttgat aatttgatat atgtatcaag tctctaatac atgtgctcat gtataattat      1920

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313 aggctgaaat atcattgtgc cgagtgtaca aaaggccagg agtagaagat catccatcgg 1980
315 taccacgttc tctctccaca agacatcata accataactc atcgacatca tcccgtttag 2040
317 ccttaagaca acaacaacac cattcatcct cctctaataca ttccgacaac aaccttaaca 2100
319 acaacaacaa catcaacaat ctcgagaagc tctccaccga atattccggc gacggcagca 2160
321 caacaacaac gaccacaaac agtaactctg acgttaccat tgctctagcc aatcaaaaaca 2220
323 tatatcgctc aatgccttac gacacaagca acaacacatt gatagtctct acgagaaatc 2280
325 atcaagacga tgatgaaact gccattgttg acgatcttca aagactagtt aactaccaaa 2340
327 tatcagatgg aggtaacatc aatcaccaat actttcaaat tgctcaacag ttcatcata 2400
329 ctcaacaaca aaatgctaac gcaaacgcat tacaattggg ggctgcggcg actacagcga 2460
331 caacgctaata gcctcaaaact caagcggcgt tagctatgaa catgattcct gcaggaacga 2520
333 ttccaaacaa tgctttgtgg gatatgtgga atccaatagt accagatgga aacagagatc 2580
335 actatactaa tattcctttt aagtaa 2606

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341 <213> ORGANISM: Artificial Sequence
343 <220> FEATURE:
344 <223> OTHER INFORMATION: Sense primer of LOV1
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350 <210> SEQ ID NO: 5
351 <211> LENGTH: 31
352 <212> TYPE: DNA
353 <213> ORGANISM: Artificial Sequence
355 <220> FEATURE:
356 <223> OTHER INFORMATION: Antisense primer of LOV1
358 <400> SEQUENCE: 5
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362 <210> SEQ ID NO: 6
363 <211> LENGTH: 27
364 <212> TYPE: DNA
365 <213> ORGANISM: Artificial Sequence
367 <220> FEATURE:
368 <223> OTHER INFORMATION: Sense primer of FLC
370 <400> SEQUENCE: 6
371 cccgttaact gaacccaaac ctgagga 27
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375 <211> LENGTH: 24
376 <212> TYPE: DNA
377 <213> ORGANISM: Artificial Sequence
379 <220> FEATURE:
380 <223> OTHER INFORMATION: Antisense primer of FLC
382 <400> SEQUENCE: 7
383 ccactagtcg cccttatcag cgga 24
386 <210> SEQ ID NO: 8
387 <211> LENGTH: 27
388 <212> TYPE: DNA
389 <213> ORGANISM: Artificial Sequence
391 <220> FEATURE:

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/780,703A

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